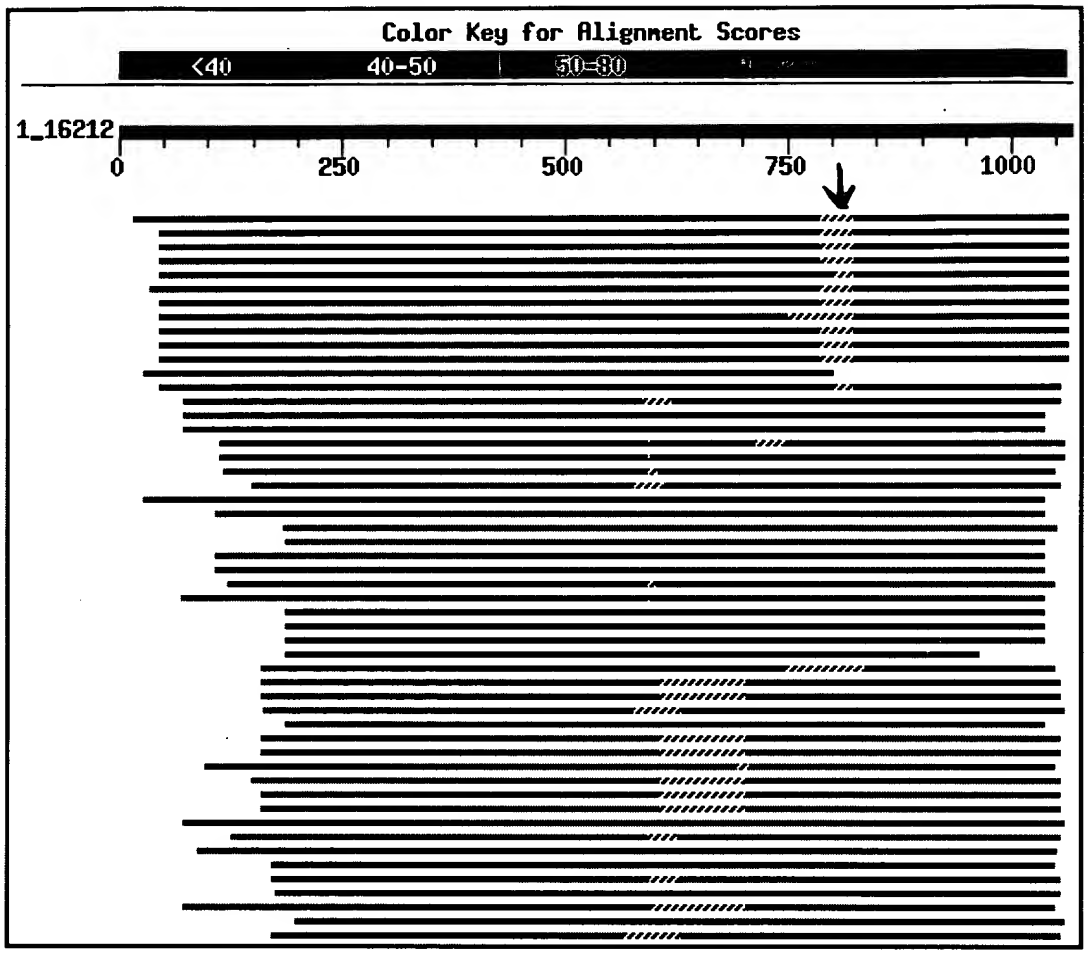


6

Sequences producing significant alignments:	Score (bits)	E Value	
gi|1438904|gb|AAC50623.1| 5-HT4L receptor >gi|2494993|sp|Q1...	410	e-113	G
gi|32481997|gb|AAP84351.1| neuropeptide Y receptor Y5 [Homo...	389	e-107	G
gi|11875770|gb|AAG40773.1| neuropeptide Y receptor Y5 [Maca...	389	e-107	
gi|14029710|gb|AAK52800.1| NPY receptor 5 [Cavia porcellus]	380	e-104	
gi|50978824|ref|NP_001003118.1| neuropeptide Y receptor typ...	379	e-104	G
gi|1438906|gb|AAC52677.1| 5-HT4L receptor >gi|2494994|sp|Q6...	364	2e-99	G
gi|4249729|gb|AAD13778.1| neuropeptide Y5 receptor [Sus scr...	360	3e-98	
gi|6981284|ref|NP_037001.1| neuropeptide Y receptor Y5; Neu...	360	3e-98	G
gi|2564651|gb|AAB81829.1| neuropeptide Y Y5 receptor [Mus m...	350	3e-95	G
gi|7710072|ref|NP_057917.1| neuropeptide Y receptor Y5 [Mus...	350	3e-95	G
gi|3169285|gb|AAC17839.1| neuropeptide Y receptor type 5 [M...	348	1e-94	G
gi|50746172|ref|XP_420388.1| PREDICTED: similar to neuropep...	281	2e-74	G
gi|19548984|gb|AAK83556.1| neuropeptide Y receptor Y5 [Gall...	271	3e-71	
gi|33302263|gb|AAO62565.1| NPY receptor Y1 [Squalus acanthias]	116	5e-57	
gi|19548986|gb|AAK83557.1| neuropeptide Y receptor Y1 [Gall...	118	3e-55	
gi|33302259|gb|AAO62564.1| NPY receptor Y6 [Squalus acanthias]	108	2e-53	
gi|2134119|pir||S71152 neuropeptide Y/peptide YY receptor Y...	114	3e-53	G
gi|50746252|ref|XP_426285.1| PREDICTED: similar to neuropep...	118	5e-53	G
gi|47523648|ref|NP_999453.1| neuropeptide Y Y1 receptor [Su...	118	5e-52	G

gi|6457648|gb|AAD13776.2| neuropeptide Y1 receptor [Sus scr...	118	5e-52	G
gi|18859127|ref|NP_571515.1| neuropeptide Y/peptide YY rece...	124	9e-52	G
gi|50950123|ref|NP_001002930.1| neuropeptide Y receptor Y1 ...	116	3e-51	G
gi|4505445|ref|NP_000900.1| neuropeptide Y receptor Y1 [Hom...	114	1e-50	G
gi|11875766|gb|AAG40771.1| neuropeptide Y receptor Y1 [Maca...	114	1e-50	
gi|5410446|gb|AAD43060.1| neuropeptide Y receptor Y1 [Cavia...	115	2e-50	
gi|34877858|ref|XP_344503.1| neuropeptide Y receptor Y1 [Ra...	116	4e-50	G
gi|189154|gb|AAA59920.1| neuropeptide y receptor	112	6e-50	G
gi|57637|emb|CAA77579.1| NPY-1 receptor [Rattus rattus] >gi...	115	8e-50	G
gi|111640|pir||S12863 G protein-coupled receptor FC5 - rat ...	115	8e-50	
gi|30410856|gb|AAH51420.1| Npy1r protein [Mus musculus] >gi...	114	1e-49	G
gi|4106397|gb|AAD02833.1| neuropeptide Y/peptide YY recepto...	102	1e-45	
gi|6754884|ref|NP_035065.1| neuropeptide Y receptor Y6 [Mus...	105	1e-45	G
gi|18253297|gb|AAL66410.1| NPY receptor [Lampetra fluviatilis]	118	3e-44	
gi|33302257|gb|AAO62563.1| NPY receptor Y4 [Squalus acanthias]	114	2e-43	
gi|19071213|gb|AAL84161.1| neuropeptide Y receptor 4 [Gallu...	108	5e-43	
gi|37778942|gb|AAN78328.1| neuropeptide Y receptor Y6 [Peca...	100	2e-42	
gi|50746142|ref|XP_420373.1| PREDICTED: similar to neuropep...	112	3e-40	G
gi|11545537|gb|AAG37898.1| neuropeptide Y receptor Y2 [Gall...	112	3e-40	
gi|49456855|emb|CAG46748.1| PPYR1 [Homo sapiens]	113	5e-40	G
gi|46410163|gb|AAS93941.1| NPY receptor Y7 [Danio rerio]	112	5e-40	
gi|50749562|ref|XP_426511.1| PREDICTED: similar to neuropep...	97	1e-39	G
gi|47217601|emb|CAG02528.1| unnamed protein product [Tetrao...	94	2e-39	
gi|18859129|ref|NP_571511.1| neuropeptide Y/peptide YY rece...	105	3e-39	G
gi|7417238|gb|AAF62507.1| neuropeptide Y-family receptor Y4...	111	4e-39	G
gi|4235257|gb|AAD13143.1| neuropeptide Y receptor type 2 [C...	111	5e-39	
gi|51452114|gb|AAH75053.2| Neuropeptide Y receptor Y2 [Homo...	111	7e-39	G
gi|961480|dbj|BAA09888.1| neuropeptide Y-Y1beta receptor [M...	114	7e-39	G
gi|1314330|gb|AAB07760.1| neuropeptide y/peptide YY recepto...	110	1e-38	G
gi|6679122|ref|NP_032757.1| neuropeptide Y receptor Y2; NPY...	111	1e-38	G
gi|26340626|dbj|BAC33975.1| unnamed protein product [Mus mu...	111	1e-38	G
gi|50755049|ref|XP_414599.1| PREDICTED: similar to NPY rece...	117	2e-38	G
gi|13027422|ref|NP_076458.1| neuropeptide Y receptor Y2; ne...	110	2e-38	G
gi|1000751|gb|AAA93170.1| type 2 neuropeptide Y receptor	109	2e-38	G
gi|4249727|gb|AAD13777.1| neuropeptide Y2 receptor [Sus scr...	112	3e-38	
gi|27806023|ref|NP_776826.1| neuropeptide Y receptor Y2 [Bo...	110	3e-38	G
gi|13928788|ref|NP_113769.1| pancreatic polypeptide recepto...	112	3e-38	G
gi|1109769|emb|CAA92322.1| pancreatic polypeptide receptor ...	112	3e-38	G
gi|47523392|ref|NP_999315.1| neuropeptide Y Y2 receptor [Su...	111	3e-38	G
gi|11875768|gb|AAG40772.1| neuropeptide Y receptor Y2 [Maca...	110	4e-38	
gi|4098212|gb|AAD00248.1| neuropeptide Y receptor type 2 [H...	111	1e-37	G
gi|4235259|gb|AAD13144.1| pancreatic polypeptide receptor Y...	105	2e-37	
gi|18859131|ref|NP_571512.1| neuropeptide Y/peptide YY rece...	105	6e-37	G
gi|47228590|emb|CAG05410.1| unnamed protein product [Tetrao...	100	5e-36	
gi|4758474|ref|NP_004239.1| G protein-coupled receptor 10; ...	100	2e-35	G
gi|31239533|ref|XP_320180.1| ENSANGP00000011806 [Anopheles ...	98	4e-35	G
gi|47223673|emb|CAF99282.1| unnamed protein product [Tetrao...	92	2e-34	
gi|1002739|gb|AAC50504.1| GPR10	94	3e-33	G
gi|50749931|ref|XP_426542.1| PREDICTED: similar to Prolacti...	92	8e-33	G

gi|47228890|emb|CAG09405.1| unnamed protein product [Tetrao...	110	1e-32	
gi|31208067|ref|XP_313000.1| ENSANGP00000020441 [Anopheles ...	88	2e-30	G
gi|17945440|gb|AAL48774.1| RE18294p [Drosophila melanogaster]	91	8e-30	
gi|28571531|ref|NP_524245.3| CG1147-PA [Drosophila melanoga...	91	8e-30	G
gi|13937102|gb|AAK50050.1| neuropeptide F receptor [Drosoph...	91	8e-30	
gi|38087207|ref|XP_142008.2| similar to G protein-coupled r...	105	1e-29	G
gi|34880717|ref|XP_231463.2| similar to G protein-coupled r...	106	3e-29	G
gi|50745619|ref|XP_426254.1| PREDICTED: similar to G protei...	93	1e-28	G
gi|1679632|gb|AAB19187.1| truncated pancreatic polypeptide ...	100	2e-28	
gi|50731261|ref|XP_425651.1| PREDICTED: similar to G protei...	96	2e-28	G
gi|1731790|dbj|BAA13103.1| Y6 encoding protein [Homo sapiens]	100	4e-28	
gi|1857635|gb|AAD11810.1| lymnokinin receptor [Lymnaea stag...	97	2e-27	
gi|5420385|emb|CAA57620.1| G protein-coupled receptor 105 [...	83	4e-27	
gi|85080|pir||A41738 neuropeptide Y receptor - fruit fly (D...	94	4e-27	
gi|24643096|ref|NP_523404.2| CG6857-PA [Drosophila melanoga...	106	7e-27	G
gi|51092236|gb|AAT94531.1| AT16733p [Drosophila melanogaster]	93	7e-27	
gi|45549233|ref|NP_524525.3| CG5811-PA [Drosophila melanoga...	93	7e-27	G
gi|25152230|ref|NP_509725.2| neuropeptide receptor NPR1 (46...	77	7e-27	G
gi|7959347|dbj|BAA96064.1| KIAA1540 protein [Homo sapiens]	97	2e-26	G
gi|45768492|gb|AAH67473.1| G protein-coupled receptor 83 [H...	97	2e-26	G
gi|33354257|ref|NP_057624.2| G protein-coupled receptor 83;...	97	2e-26	G
gi|7248882|gb|AAF43705.1| orphan G-protein coupled receptor...	97	2e-26	G
gi|50978808|ref|NP_001003108.1| glucocorticoid induced rece...	97	2e-26	G
gi|34860282|ref|XP_346816.1| hypothetical protein XP_346815...	96	6e-26	G
gi|14028711|gb|AAK52473.1| allatostatin receptor [Periplane...	88	8e-26	
gi|25388079|pir||JC7677 allatostatin receptor - American co...	88	8e-26	
gi|2707338|gb|AAB92258.1| cardioexcitatory receptor [Lymnae...	78	8e-26	
gi|45767703|gb|AAH67474.1| G protein-coupled receptor 83 [H...	94	1e-25	G
gi|48139558|ref|XP_397024.1| similar to allatostatin recept...	93	1e-25	G
gi|14279167|gb|AAK58514.1| G-protein-coupled receptor 74 [M...	96	1e-25	G
gi|6753988|ref|NP_034417.1| G protein-coupled receptor 83; ...	94	1e-25	G
gi|45383432|ref|NP_989693.1| neuropeptide FF 1, RFamide-rel...	98	1e-25	G

Alignments

Get selected sequences | Select all | Deselect all

☐ >gi|1438904|gb|AAC50623.1| G 5-HT4L receptor
gi|2494993|sp|Q15761|NY5R_HUMAN G Neuropeptide Y receptor type 5 (NPY5-R) (NPY-Y5 receptor) (NPYY5)
Length = 455

Score = 410 bits (1054), Expect = e-113
Identities = 212/263 (80%), Positives = 227/263 (86%), Gaps = 7/263 (2%)
Frame = +2

```
Query: 17  MSFYSKQDYNMDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTF 196
           MSFYSKQDYNMDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTF
Sbjct: 1   MSFYSKQDYNMDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTF 60
```

```
Query: 197 VSLLGFMGNLLILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFG 376
           VSLLGFMGNLLILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFG
Sbjct: 61  VSLLGFMGNLLILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFG 120

Query: 377 KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAI 556
           KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAI
Sbjct: 121 KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAI 180

Query: 557 CSPLPVFHSLVELQETFGSALLAAGIYVL----SHGHLIHTELPLLSLYC*FSYSALSLS 724
           CSPLPVFHSLVELQETFGSALL++    +    S  + I    + LL +         L++S
Sbjct: 181 CSPLPVFHSLVELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVS 240

Query: 725 Y---CKSYKCLHTPKKEKQHDGQ 784
           +   C+S  C  + K+ +  + +
Sbjct: 241 HTSVCRSISCGLSNKENRLEENE 263
```

```
 Score =  172 bits (437), Expect = 1e-41
 Identities = 80/80 (100%), Positives = 80/80 (100%)
 Frame = +3
```

```
Query: 825  VFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCLNPILY 1004
           VFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCLNPILY
Sbjct: 376  VFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCLNPILY 435

Query: 1005 GFLNNGIKADLVSLIHCLHM 1064
           GFLNNGIKADLVSLIHCLHM
Sbjct: 436  GFLNNGIKADLVSLIHCLHM 455
```

```
 Score = 60.5 bits (145), Expect(2) = 2e-12
 Identities = 28/34 (82%), Positives = 30/34 (88%)
 Frame = +1
```

```
Query: 613 SIASSRYLCVESWPSDSYRIAFTISLLLVQLFCP 714
           ++ SSRYLCVESWPSDSYRIAFTISLLLVQ   P
Sbjct: 200 ALLSSRYLCVESWPSDSYRIAFTISLLLVQYILP 233
```

```
 Score = 35.0 bits (79), Expect(2) = 2e-12
 Identities = 15/15 (100%), Positives = 15/15 (100%)
 Frame = +3
```

```
Query: 705 ILPLVCLTVSHTSVC 749
           ILPLVCLTVSHTSVC
Sbjct: 231 ILPLVCLTVSHTSVC 245
```

☐ >gi|32481997|gb|AAP84351.1| G neuropeptide Y receptor Y5 [Homo sapiens]
gi|5453796|ref|NP_006165.1| G neuropeptide Y receptor Y5 [Homo sapiens]
gi|27502796|gb|AAH42416.1| G Neuropeptide Y receptor Y5 [Homo sapiens]
gi|1945449|gb|AAC51295.1| G neuropeptide Y5 receptor [Homo sapiens]
gi|1620656|gb|AAC50741.1| G neuropeptide Y5 receptor
Length = 445

```
 Score =  389 bits (999), Expect = e-107
 Identities = 202/253 (79%), Positives = 217/253 (85%), Gaps = 7/253 (2%)
 Frame = +2

Query: 47  MDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGFMGNL 226
           MDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGFMGNL
Sbjct: 1   MDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGFMGNL 60

Query: 227 LILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFGKVMCHIMPFL 406
           LILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFGKVMCHIMPFL
Sbjct: 61  LILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFGKVMCHIMPFL 120

Query: 407 QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSL 586
           QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSL
Sbjct: 121 QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSL 180

Query: 587 VELQETFGSALLAAGIYVL----SHGHLIHTELPLLSLYC*FSYSALSLSY---CKSYKC 745
           VELQETFGSALL++    +    S  + I   + LL +        L++S+   C+S  C
Sbjct: 181 VELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVSHTSVCRSISC 240

Query: 746 LHTPKKEKQHDGQ 784
             + K+ +  + +
Sbjct: 241 GLSNKENRLEENE 253


 Score =  172 bits (437), Expect = 1e-41
 Identities = 80/80 (100%), Positives = 80/80 (100%)
 Frame = +3

Query: 825  VFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCLNPILY 1004
           VFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCLNPILY
Sbjct: 366  VFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCLNPILY 425

Query: 1005 GFLNNGIKADLVSLIHCLHM 1064
           GFLNNGIKADLVSLIHCLHM
Sbjct: 426  GFLNNGIKADLVSLIHCLHM 445


 Score = 60.5 bits (145), Expect(2) = 2e-12
 Identities = 28/34 (82%), Positives = 30/34 (88%)
 Frame = +1

Query: 613 SIASSRYLCVESWPSDSYRIAFTISLLLVQLFCP 714
           ++ SSRYLCVESWPSDSYRIAFTISLLLVQ   P
Sbjct: 190 ALLSSRYLCVESWPSDSYRIAFTISLLLVQYILP 223


 Score = 35.0 bits (79), Expect(2) = 2e-12
 Identities = 15/15 (100%), Positives = 15/15 (100%)
 Frame = +3

Query: 705 ILPLVCLTVSHTSVC 749
           ILPLVCLTVSHTSVC
Sbjct: 221 ILPLVCLTVSHTSVC 235
```

☐ >gi|11875770|gb|AAG40773.1| neuropeptide Y receptor Y5 [Macaca mulatta]
Length = 445

Score = 389 bits (999), Expect = e-107
Identities = 202/253 (79%), Positives = 217/253 (85%), Gaps = 7/253 (2%)
Frame = +2

```
Query: 47  MDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGFMGNL 226
           MDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGFMGNL
Sbjct: 1   MDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGFMGNL 60

Query: 227 LILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFGKVMCHIMPFL 406
           LILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFGKVMCHIMPFL
Sbjct: 61  LILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFGKVMCHIMPFL 120

Query: 407 QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSL 586
           QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSL
Sbjct: 121 QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSL 180

Query: 587 VELQETFGSALLAAGIYVL----SHGHLIHTELPLLSLYC*FSYSALSLSY---CKSYKC 745
           VELQETFGSALL++    +    S  + I   + LL +        L++S+   C+S  C
Sbjct: 181 VELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVSHTSVCRSISC 240

Query: 746 LHTPKKEKQHDGQ 784
             + K+ +  + +
Sbjct: 241 GLSNKENRLEENE 253
```

Score = 171 bits (434), Expect = 2e-41
Identities = 79/80 (98%), Positives = 80/80 (100%)
Frame = +3

```
Query: 825  VFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCLNPILY 1004
           VFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCLNPILY
Sbjct: 366  VFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCLNPILY 425

Query: 1005 GFLNNGIKADLVSLIHCLHM 1064
           GFLNNGIKADL+SLIHCLHM
Sbjct: 426  GFLNNGIKADLMSLIHCLHM 445
```

Score = 60.5 bits (145), Expect(2) = 2e-12
Identities = 28/34 (82%), Positives = 30/34 (88%)
Frame = +1

```
Query: 613 SIASSRYLCVESWPSDSYRIAFTISLLLVQLFCP 714
           ++ SSRYLCVESWPSDSYRIAFTISLLLVQ   P
Sbjct: 190 ALLSSRYLCVESWPSDSYRIAFTISLLLVQYILP 223
```

Score = 35.0 bits (79), Expect(2) = 2e-12
Identities = 15/15 (100%), Positives = 15/15 (100%)
Frame = +3

```
Query: 705 ILPLVCLTVSHTSVC 749
           ILPLVCLTVSHTSVC
```

```
Sbjct: 221 ILPLVCLTVSHTSVC 235
```

☐ >gi|14029710|gb|AAK52800.1| NPY receptor 5 [Cavia porcellus]
Length = 446

```
 Score =  380 bits (977), Expect = e-104
 Identities = 197/253 (77%), Positives = 214/253 (84%), Gaps = 7/253 (2%)
 Frame = +2

Query: 47  MDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGFMGNL 226
           MDLEL EYYNKTLATENNT  TRNSDFPVWDDY+SSVDDLQYFLIGLYTFVSLLGFMGNL
Sbjct: 1   MDLELKEYYNKTLATENNTTTTRNSDFPVWDDYRSSVDDLQYFLIGLYTFVSLLGFMGNL 60

Query: 227 LILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFGKVMCHIMPFL 406
           LILMAL+KKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFGKVMCHIMPFL
Sbjct: 61  LILMALIKKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFGKVMCHIMPFL 120

Query: 407 QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSL 586
           QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSL
Sbjct: 121 QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSL 180

Query: 587 VELQETFGSALLAAGIYVL----SHGHLIHTELPLLSLYC*FSYSALSLSY---CKSYKC 745
           VELQETFGSALL++    +    S  + I   + LL +        L++S+   C+S  C
Sbjct: 181 VELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVSHTSVCRSISC 240

Query: 746 LHTPKKEKQHDGQ 784
             + K+ +  + +
Sbjct: 241 GLSNKENRLEENE 253
```

```
 Score =  170 bits (431), Expect = 5e-41
 Identities = 78/80 (97%), Positives = 80/80 (100%)
 Frame = +3

Query: 825  VFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCLNPILY 1004
           VFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCLNPILY
Sbjct: 366  VFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCLNPILY 425

Query: 1005 GFLNNGIKADLVSLIHCLHM 1064
           GFLNNGIKADL+SLIHCLH+
Sbjct: 426  GFLNNGIKADLMSLIHCLHL 445
```

```
 Score = 60.5 bits (145), Expect(2) = 2e-12
 Identities = 28/34 (82%), Positives = 30/34 (88%)
 Frame = +1

Query: 613 SIASSRYLCVESWPSDSYRIAFTISLLLVQLFCP 714
           ++ SSRYLCVESWPSDSYRIAFTISLLLVQ   P
Sbjct: 190 ALLSSRYLCVESWPSDSYRIAFTISLLLVQYILP 223
```

```
 Score = 35.0 bits (79), Expect(2) = 2e-12
 Identities = 15/15 (100%), Positives = 15/15 (100%)
 Frame = +3
```

```
Query: 705 ILPLVCLTVSHTSVC 749
           ILPLVCLTVSHTSVC
Sbjct: 221 ILPLVCLTVSHTSVC 235
```

☐ >gi|50978824|ref|NP_001003118.1| G neuropeptide Y receptor type 5 [Canis familia
gi|3169283|gb|AAC17838.1| G neuropeptide Y receptor type 5 [Canis familiaris]
gi|3914178|sp|O62729|NY5R_CANFA Neuropeptide Y receptor type 5 (NPY5-R) (NPY-Y5 r
receptor) (NPYY5)
Length = 446

```
 Score =  379 bits (973), Expect = e-104
 Identities = 197/253 (77%), Positives = 214/253 (84%), Gaps = 7/253 (2%)
 Frame = +2

Query: 47  MDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGFMGNL 226
           MDLEL ++YNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGFMGNL
Sbjct: 1   MDLELQDFYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGFMGNL 60

Query: 227 LILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFGKVMCHIMPFL 406
           LILMALM+KRNQKT VNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFGKVMCHIMPFL
Sbjct: 61  LILMALMRKRNQKTMVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFGKVMCHIMPFL 120

Query: 407 QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSL 586
           QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSL
Sbjct: 121 QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSL 180

Query: 587 VELQETFGSALLAAGIYVL----SHGHLIHTELPLLSLYC*FSYSALSLSY---CKSYKC 745
           VELQETF SALL++    +    S  + I   + LL +        L++S+   C+S  C
Sbjct: 181 VELQETFDSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVSHTSVCRSISC 240

Query: 746 LHTPKKEKQHDGQ 784
             + K+ K  + +
Sbjct: 241 GLSNKENKLEENE 253
```

```
 Score =  169 bits (428), Expect = 1e-40
 Identities = 78/80 (97%), Positives = 79/80 (98%)
 Frame = +3

Query: 825  VFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCLNPILY 1004
           VFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCLNPILY
Sbjct: 366  VFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCLNPILY 425

Query: 1005 GFLNNGIKADLVSLIHCLHM 1064
           GFLNNGIKADL+SLI CLHM
Sbjct: 426  GFLNNGIKADLISLIQCLHM 445
```

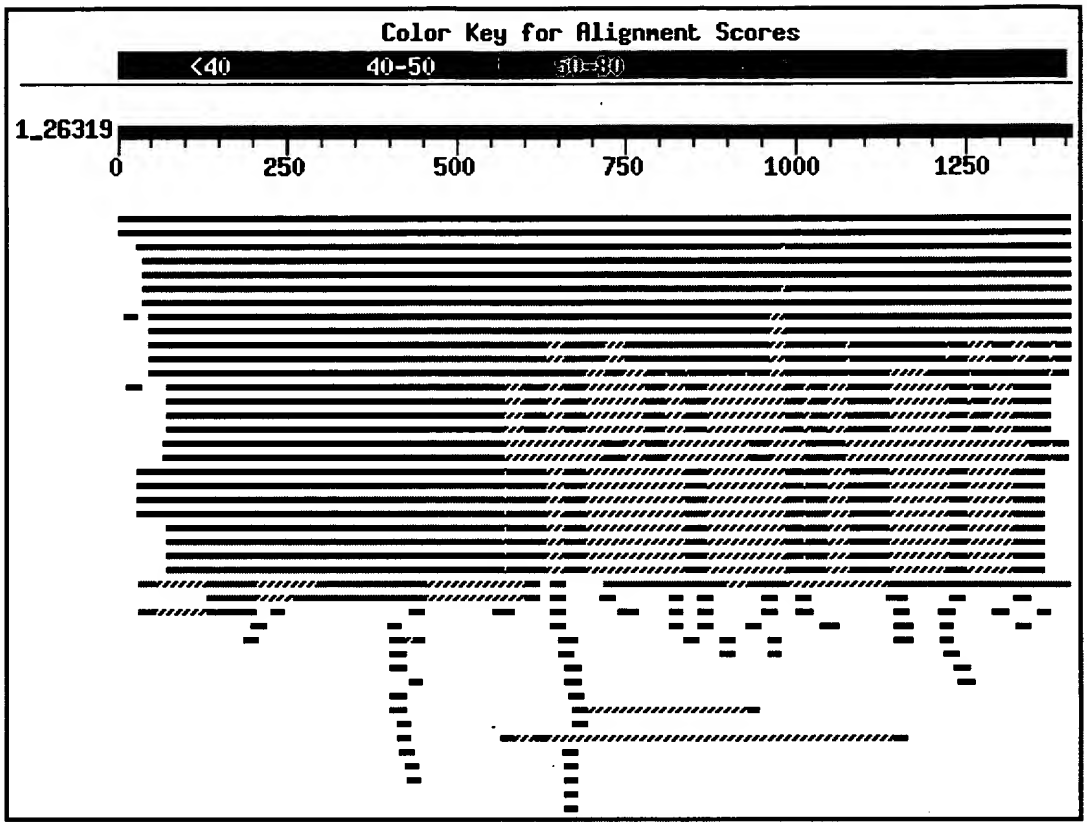
```
 Score = 60.5 bits (145), Expect(2) = 1e-12
 Identities = 28/34 (82%), Positives = 30/34 (88%)
 Frame = +1

Query: 613 SIASSRYLCVESWPSDSYRIAFTISLLLVQLFCP 714
           ++ SSRYLCVESWPSDSYRIAFTISLLLVQ   P
```

```
Sbjct: 190 ALLSSRYLCVESWPSDSYRIAFTISLLLVQYILP 223


 Score = 36.2 bits (82), Expect(2) = 1e-12
 Identities = 18/33 (54%), Positives = 24/33 (72%), Gaps = 1/33 (3%)
 Frame = +3

Query: 705 ILPLVCLTVSHTSVCIRLK-RRNNMMDKMRDNK 800
           ILPLVCLTVSHTSVC  +    +N  +K+ +N+
Sbjct: 221 ILPLVCLTVSHTSVCRSISCGLSNKENKLEENE 253
```

☐ >gi|1438906|gb|AAC52677.1| G 5-HT4L receptor

gi|2494994|sp|Q63634|NY5R_RAT G Neuropeptide Y receptor type 5 (NPY5-R) (NPY-Y5 r
receptor)
Length = 456

```
 Score =  364 bits (934), Expect = 2e-99
 Identities = 186/257 (72%), Positives = 212/257 (82%), Gaps = 7/257 (2%)
 Frame = +2

Query: 35  QDYNMDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGF 214
           QD +M+ +L+E++NKT  TENNTAA RN+ FP W+DY+ SVDDLQYFLIGLYTFVSLLGF
Sbjct: 8   QDSSMEFKLEEHFNKTFVTENNTAAARNAAFPAWEDYRGSVDDLQYFLIGLYTFVSLLGF 67

Query: 215 MGNLLILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFGKVMCHI 394
           MGNLLILMA+MKKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFGK MCHI
Sbjct: 68  MGNLLILMAVMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFGKAMCHI 127

Query: 395 MPFLQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPV 574
           MPFLQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPV
Sbjct: 128 MPFLQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPV 187

Query: 575 FHSLVELQETFGSALLAAGIYVL----SHGHLIHTELPLLSLYC*FSYSALSLSY---CK 733
           FHSLVEL+ETFGSALL++    +    S  + I   + LL +         L++S+   C+
Sbjct: 188 FHSLVELKETFGSALLSSKYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVSHTSVCR 247

Query: 734 SYKCLHTPKKEKQHDGQ 784
           S  C  + K+ +  + +
Sbjct: 248 SISCGLSHKENRLEENE 264


 Score =  167 bits (424), Expect = 3e-40
 Identities = 77/80 (96%), Positives = 79/80 (98%)
 Frame = +3

Query: 825  VFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCLNPILY 1004
            VFYRLTILILVFAVSWMPLH+FHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCLNPILY
Sbjct: 376  VFYRLTILILVFAVSWMPLHVFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCLNPILY 435

Query: 1005 GFLNNGIKADLVSLIHCLHM 1064
           GFLNNGIKADL +LIHCLHM
Sbjct: 436  GFLNNGIKADLRALIHCLHM 455
```



1406

Sequences producing significant alignments:	Score (bits)	E Value	
gi|16756377|gb|AC079238.7| Homo sapiens BAC clone RP11-719L...	1132	0.0	
gi|1438903|gb|U56079.1|HSU56079 Human Y5 receptor mRNA, com...	1132	0.0	G U
gi|1620655|gb|U66275.1|HSU66275 Human neuropeptide Y5 recep...	1074	0.0	G U
gi|22832895|gb|BC034224.1| Homo sapiens neuropeptide Y rece...	1059	0.0	G U
gi|31377784|ref|NM_006174.2| Homo sapiens neuropeptide Y re...	1059	0.0	G U E
gi|27502795|gb|BC042416.1| Homo sapiens neuropeptide Y rece...	1059	0.0	G U
gi|1945448|gb|U94320.1|HSU94320 Human neuropeptide Y5 recep...	1059	0.0	G U E
gi|32481996|gb|AY322538.1| Homo sapiens neuropeptide Y rece...	1041	0.0	G
gi|11875769|gb|AF303091.1|AF303091 Macaca mulatta neuropept...	969	0.0	
gi|50978823|ref|NM_001003118.1| Canis familiaris neuropepti...	779	0.0	G U
gi|3169282|gb|AF049328.1|AF049328 Canis familiaris neuropep...	779	0.0	G U E
gi|14029709|gb|AF363240.1|AF363240 Cavia porcellus NPY rece...	660	0.0	
gi|6981283|ref|NM_012869.1| Rattus norvegicus neuropeptide ...	545	e-152	G U E
gi|1620657|gb|U66274.1|RNU66274 Rattus norvegicus neuropept...	545	e-152	G U E
gi|1438905|gb|U56078.1|RNU56078 Rattus norvegicus Y5 recept...	545	e-152	G U
gi|3098509|gb|AF044264.1|AF044264 Rattus norvegicus neurope...	545	e-152	G U
gi|4249728|gb|AF106083.1|AF106083 Sus scrofa neuropeptide Y...	539	e-150	
gi|3808059|dbj|AB019185.1| Sus scrofa NPY Y5 gene for neuro...	539	e-150	
gi|22476189|gb|AC123796.2| Mus musculus BAC clone RP24-320P...	523	e-145	
gi|33942177|gb|AC116731.9| Mus musculus chromosome 8, clone...	523	e-145	
gi|52839799|gb|AC100541.17| Mus musculus chromosome 8, clon...	523	e-145	
gi|2564650|gb|AF022948.1|AF022948 Mus musculus neuropeptide...	523	e-145	G

[redacted]

gi|26337480|dbj|AK045587.1| Mus musculus adult male corpora...	523	e-145	G U
gi|3169284|gb|AF049329.1|AF049329 Mus musculus neuropeptide...	519	e-144	G U E
gi|7710071|ref|NM_016708.1| Mus musculus neuropeptide Y rec...	515	e-143	G U E
gi|6714644|dbj|AB001346.1| Mus musculus mRNA for neuropepti...	515	e-143	G U E
gi|50746171|ref|XM_420388.1| PREDICTED: Gallus gallus simil...	98	7e-17	G
gi|19548983|gb|AY040844.1| Gallus gallus neuropeptide Y rec...	92	4e-15	
gi|976208|gb|L47169.1|HUMNPYAC Homo sapiens neuropeptide Y ...	70	2e-08	
gi|46427829|emb|CR389184.1| Gallus gallus finished cDNA, cl...	56	2e-04	U
gi|51100952|dbj|AB104827.2| Candida boidinii FGH1 gene for ...	44	0.87	
gi|31746714|gb|AC133101.4| Mus musculus BAC clone RP23-154M...	42	3.5	
gi|37693674|gb|AC121082.13| Mus musculus chromosome 7, clon...	42	3.5	
gi|32880270|gb|AC118695.10| Mus musculus chromosome 19, clo...	42	3.5	
gi|53379715|gb|AC149588.4| Mus musculus chromosome 15 clone...	42	3.5	
gi|52077841|gb|AC132394.3| Mus musculus chromosome 6 clone ...	42	3.5	
gi|16603965|gb|AC076968.38| Homo sapiens 12 BAC RP11-686F15...	42	3.5	
gi|48675465|gb|AC132104.3| Mus musculus BAC clone RP24-364N...	42	3.5	
gi|34536220|dbj|AK128706.1| Homo sapiens cDNA FLJ46873 fis,...	42	3.5	U
gi|49170190|gb|AC124958.13| Medicago truncatula clone mth2-...	42	3.5	
gi|21955079|gb|AC104016.8| Homo sapiens chromosome 11, clon...	42	3.5	
gi|20334476|gb|AC079822.13| Homo sapiens 3 BAC RP11-413G22 ...	42	3.5	
gi|22549646|gb|AC092964.8| Homo sapiens 3 BAC RP11-423E7 (R...	42	3.5	
gi|20986479|gb|AC084701.5| Homo sapiens chromosome 18, clon...	42	3.5	
gi|2462139|emb|Z70681.1|CEC30F2 Caenorhabditis elegans cosm...	42	3.5	
gi|28173126|gb|AC100865.5| Homo sapiens chromosome 11, clon...	42	3.5	
gi|27884981|gb|AC117539.6| Papio hamadryas, clone RP41-208E...	42	3.5	
gi|15638824|gb|AC096569.1| Homo sapiens BAC clone RP11-347B...	42	3.5	
gi|14702085|gb|AC013722.8| Homo sapiens BAC clone RP11-299H...	42	3.5	
gi|15431133|gb|AC013660.9| Homo sapiens, clone RP11-20A14, ...	42	3.5	
gi|2109298|gb|AF000132.1|AHAF000132 Amaranthus hypochondria...	42	3.5	
gi|13560010|emb|AL356318.7| Human DNA sequence from clone R...	42	3.5	
gi|24366576|emb|AL808118.8| Mouse DNA sequence from clone R...	42	3.5	
gi|10280826|gb|AC012531.11|AC012531 Homo sapiens, clone RP1...	42	3.5	
gi|42491502|gb|AC102734.11| Mus musculus chromosome 6, clon...	42	3.5	
gi|608510|gb|U16311.1|BRU16311 Brachydanio rerio homeodomai...	42	3.5	G U
gi|26330583|dbj|AK035302.1| Mus musculus adult male urinary...	42	3.5	G U
gi|26084230|dbj|AK034836.1| Mus musculus 12 days embryo emb...	42	3.5	G U
gi|21211711|emb|AL359771.27| Human DNA sequence from clone ...	42	3.5	
gi|38678612|gb|AC117702.10| Mus musculus chromosome 10, clo...	40	14	
gi|17570664|ref|NM_077495.1| Caenorhabditis elegans allatos...	40	14	G
gi|28604212|gb|AC124775.4| Mus musculus BAC clone RP23-60N3...	40	14	
gi|19310330|gb|AC104789.4| Homo sapiens BAC clone RP11-138B...	40	14	
gi|48391178|gb|AY584422.1| Xantusia bezyi isolate Xbe5_Pin5...	40	14	
gi|48391102|gb|AY584384.1| Xantusia bezyi isolate Xbe2_GaL1...	40	14	
gi|34368596|gb|AC120736.4| Rattus norvegicus 11 BAC CH230-2...	40	14	
gi|33242564|gb|AY336522.1| Sulfolobus solfataricus strain P...	40	14	
gi|44844336|emb|BX247953.2| Mouse DNA sequence from clone R...	40	14	
gi|30725969|gb|AC100271.6| Mus musculus, clone RP23-77E14, ...	40	14	
gi|51233561|gb|AC110499.19| Mus musculus chromosome 1, clon...	40	14	
gi|51036712|gb|AC130808.26| Medicago truncatula clone mth2-...	40	14	
gi|50761406|ref|XM_424720.1| PREDICTED: Gallus gallus simil...	40	14	G
gi|20258986|gb|AY091270.1| Arabidopsis thaliana putative si...	40	14	G U
gi|17380917|gb|AY063915.1| Arabidopsis thaliana putative pu...	40	14	G U
gi|48675548|gb|AC134472.4| Mus musculus BAC clone RP23-123E...	40	14	
gi|46195482|gb|AC135316.15| Medicago truncatula clone mth2-...	40	14	
gi|22539131|gb|AC105009.13| Homo sapiens chromosome 8, clon...	40	14	

[redacted]

gi|21909528|gb|AC105235.7| Homo sapiens chromosome 8, clone...	40	14	
gi|34786898|emb|AL831812.5|CNS08CAP Oryza sativa chromosome...	40	14	
gi|21535755|emb|AL713907.3|CNS07YQ7 Oryza sativa chromosome...	40	14	
gi|10944453|gb|AC008752.6| Homo sapiens chromosome 19 clone...	40	14	
gi|33620400|emb|AL929018.14| Mouse DNA sequence from clone ...	40	14	
gi|21281541|gb|AC104163.2| Homo sapiens chromosome 3 clone ...	40	14	
gi|48717527|gb|AC122169.23| Medicago truncatula clone mth2-...	40	14	
gi|27228874|gb|AC093576.3| Homo sapiens chromosome 1 clone ...	40	14	
gi|49528096|emb|CR380958.1| Candida glabrata strain CBS138 ...	40	14	
gi|25137544|dbj|AP005900.1| Homo sapiens genomic DNA, chrom...	40	14	
gi|17921243|gb|AC022317.8| Homo sapiens chromosome 4 clone ...	40	14	
gi|17985904|gb|AC093581.2| Homo sapiens chromosome 1 clone ...	40	14	
gi|17155036|gb|AC091819.3| Homo sapiens chromosome 5 clone ...	40	14	
gi|24417223|dbj|AP005663.2| Homo sapiens genomic DNA, chrom...	40	14	
gi|13992802|gb|AC068551.6| Homo sapiens BAC clone RP11-720N...	40	14	
gi|16554344|gb|AC011395.5| Homo sapiens chromosome 5 clone ...	40	14	
gi|46240964|gb|AC145942.4| Gallus gallus chromosome UNK clo...	40	14	
gi|11968293|gb|AC010368.4|AC010368 Homo sapiens chromosome ...	40	14	
gi|47847914|dbj|AP004168.3| Oryza sativa (japonica cultivar...	40	14	
gi|12309635|emb|AL450428.6| Human DNA sequence from clone R...	40	14	
gi|10441989|gb|AF218030.1|AF218030 Homo sapiens clone PP79 ...	40	14	G U
gi|10441953|gb|AF218012.1|AF218012 Homo sapiens clone PP379...	40	14	G U E
gi|21734414|emb|AL833764.1|HSM805077 Homo sapiens mRNA; cDN...	40	14	G

Alignments

Get selected sequences | Select all | Deselect all

☐ >gi|16756377|gb|AC079238.7| D Homo sapiens BAC clone RP11-719L21 from 4, complet
Length = 142462

Score = 1132 bits (571), Expect = 0.0
Identities = 571/571 (100%)
Strand = Plus / Plus

```
Query: 1      ttttggttgctgacaaatgtcttttattccaagcaggactataatatggatttagagct 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 128642 ttttggttgctgacaaatgtcttttattccaagcaggactataatatggatttagagct 128701


Query: 61     cgacgagtattataacaagacacttgccacagagaataatactgctgccactcggaattc 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 128702 cgacgagtattataacaagacacttgccacagagaataatactgctgccactcggaattc 128761


Query: 121    tgatttcccagtctgggatgactataaaagcagtgtagatgacttacagtattttctgat 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 128762 tgatttcccagtctgggatgactataaaagcagtgtagatgacttacagtattttctgat 128821


Query: 181    tgggctctatacatttgtaagtcttcttggctttatggggaatctacttattttaatggc 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 128822 tgggctctatacatttgtaagtcttcttggctttatggggaatctacttattttaatggc 128881
```

```
Query: 241    tctcatgaaaaagcgtaatcagaagactacggtaaacttcctcataggcaatctggcctt 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 128882 tctcatgaaaaagcgtaatcagaagactacggtaaacttcctcataggcaatctggcctt 128941


Query: 301    ttctgatatcttggttgtgctgttttgctcacctttcacactgacgtctgtcttgctgga 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 128942 ttctgatatcttggttgtgctgttttgctcacctttcacactgacgtctgtcttgctgga 129001


Query: 361    tcagtggatgtttggcaaagtcatgtgccatattatgccttttcttcaatgtgtgtcagt 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 129002 tcagtggatgtttggcaaagtcatgtgccatattatgccttttcttcaatgtgtgtcagt 129061


Query: 421    tttggtttcaactttaattttaatatcaattgccattgtcaggtatcatatgataaaaca 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 129062 tttggtttcaactttaattttaatatcaattgccattgtcaggtatcatatgataaaaca 129121


Query: 481    tcccatatctaataatttaacagcaaaccatggctactttctgatagctactgtctggac 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 129122 tcccatatctaataatttaacagcaaaccatggctactttctgatagctactgtctggac 129181


Query: 541    actaggttttgccatctgttctcccccttcca 571
              |||||||||||||||||||||||||||||||
Sbjct: 129182 actaggttttgccatctgttctcccccttcca 129212


 Score = 69.9 bits (35), Expect = 2e-08
 Identities = 35/35 (100%)
 Strand = Plus / Plus


Query: 810    cagatgttcatgaattgagagtaaaacgttctgtt 844
              |||||||||||||||||||||||||||||||||||
Sbjct: 129721 cagatgttcatgaattgagagtaaaacgttctgtt 129755


 Score = 65.9 bits (33), Expect = 2e-07
 Identities = 33/33 (100%)
 Strand = Plus / Plus


Query: 1254   ttctgttacaagaataaaaaagagatctcgaag 1286
              |||||||||||||||||||||||||||||||||
Sbjct: 129749 ttctgttacaagaataaaaaagagatctcgaag 129781


 Score = 63.9 bits (32), Expect = 9e-07
 Identities = 32/32 (100%)
 Strand = Plus / Plus


Query: 1346   tgatgtcctgttgtcttaatccaattctatat 1377
```

```
              ||||||||||||||||||||||||||||||||
Sbjct: 129931 tgatgtcctgttgtcttaatccaattctatat 129962


 Score = 63.9 bits (32), Expect = 9e-07
 Identities = 32/32 (100%)
 Strand = Plus / Plus


Query: 1316   acaatcttatttcaaataggcatttcaagttg 1347
              ||||||||||||||||||||||||||||||||
Sbjct: 129871 acaatcttatttcaaataggcatttcaagttg 129902


 Score = 63.9 bits (32), Expect = 9e-07
 Identities = 32/32 (100%)
 Strand = Plus / Plus


Query: 719    cacagaagaagatatagcaagaagacagcatg 750
              ||||||||||||||||||||||||||||||||
Sbjct: 129540 cacagaagaagatatagcaagaagacagcatg 129571


 Score = 61.9 bits (31), Expect = 4e-06
 Identities = 31/31 (100%)
 Strand = Plus / Plus


Query: 1376   atttagtgtcccttatacactgtcttcatat 1406
              |||||||||||||||||||||||||||||||
Sbjct: 129991 atttagtgtcccttatacactgtcttcatat 130021


 Score = 61.9 bits (31), Expect = 4e-06
 Identities = 31/31 (100%)
 Strand = Plus / Plus


Query: 1287   agtatttgctgttagttggatgccactacac 1317
              |||||||||||||||||||||||||||||||
Sbjct: 129812 agtatttgctgttagttggatgccactacac 129842


 Score = 61.9 bits (31), Expect = 4e-06
 Identities = 31/31 (100%)
 Strand = Plus / Plus


Query: 1226   cttgctttgagataaaacctgaagaaaattc 1256
              |||||||||||||||||||||||||||||||
Sbjct: 129691 cttgctttgagataaaacctgaagaaaattc 129721
```

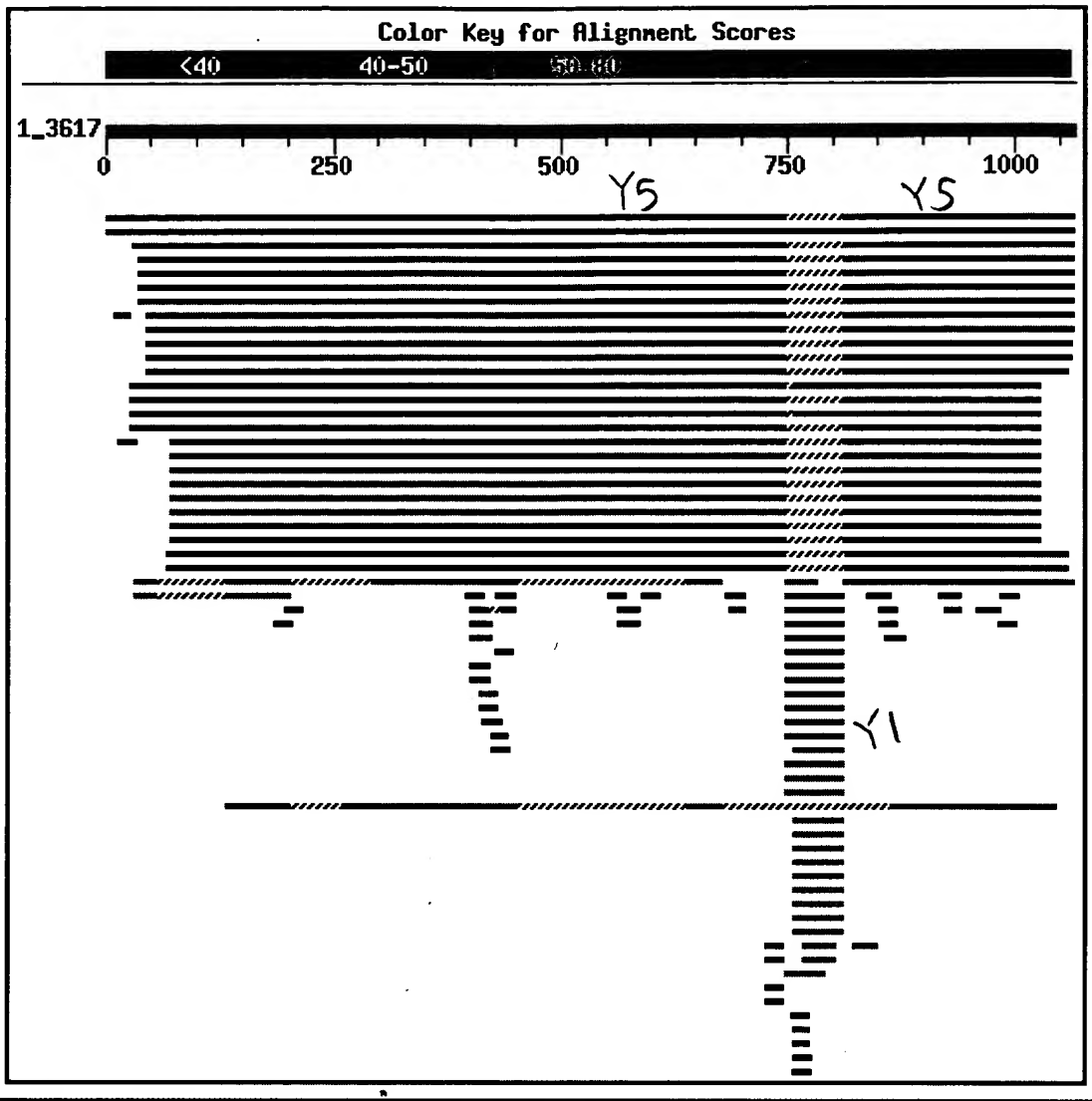
[redacted]

```
 Score = 61.9 bits (31), Expect = 4e-06
 Identities = 31/31 (100%)
 Strand = Plus / Plus


Query: 1196   actttggctctgtaagaagtcagctctcttc 1226
              ||||||||||||||||||||||||||||||
Sbjct: 129631 actttggctctgtaagaagtcagctctcttc 129661


 Score = 61.9 bits (31), Expect = 4e-06
 Identities = 31/31 (100%)
 Strand = Plus / Plus


Query: 1107   caacttaactcttcatccatccaaaaagagt 1137
              ||||||||||||||||||||||||||||||
Sbjct: 129452 caacttaactcttcatccatccaaaaagagt 129482


 Score = 61.9 bits (31), Expect = 4e-06
 Identities = 31/31 (100%)
 Strand = Plus / Plus


Query: 630    tttgtcttactgtaagtcatacaagtgtctg 660
              ||||||||||||||||||||||||||||||
Sbjct: 129361 tttgtcttactgtaagtcatacaagtgtctg 129391


 Score = 60.0 bits (30), Expect = 1e-05
 Identities = 30/30 (100%)
 Strand = Plus / Plus


Query: 931    tgggtttcttaataatgggattaaagctga 960
              ||||||||||||||||||||||||||||||
Sbjct: 129962 tgggtttcttaataatgggattaaagctga 129991


 Score = 60.0 bits (30), Expect = 1e-05
 Identities = 30/30 (100%)
 Strand = Plus / Plus


Query: 901    ggtgtattgcatttgtcatttgttgggcat 930
              ||||||||||||||||||||||||||||||
Sbjct: 129902 ggtgtattgcatttgtcatttgttgggcat 129931


 Score = 60.0 bits (30), Expect = 1e-05
 Identities = 30/30 (100%)
 Strand = Plus / Plus
```

```
Query: 871    ccttttccatgtggtaactgattttaatga 900
              ||||||||||||||||||||||||||||||
Sbjct: 129842 ccttttccatgtggtaactgattttaatga 129871


 Score = 60.0 bits (30), Expect = 1e-05
 Identities = 30/30 (100%)
 Strand = Plus / Plus


Query: 841    tgttttctacagactgaccatactgatatt 870
              ||||||||||||||||||||||||||||||
Sbjct: 129782 tgttttctacagactgaccatactgatatt 129811


 Score = 60.0 bits (30), Expect = 1e-05
 Identities = 30/30 (100%)
 Strand = Plus / Plus


Query: 781    atccagtaagttcataccaggggtccccac 810
              ||||||||||||||||||||||||||||||
Sbjct: 129662 atccagtaagttcataccaggggtccccac 129691


 Score = 60.0 bits (30), Expect = 1e-05
 Identities = 30/30 (100%)
 Strand = Plus / Plus


Query: 751    agagaaccactccagaatacttccagaaaa 780
              ||||||||||||||||||||||||||||||
Sbjct: 129602 agagaaccactccagaatacttccagaaaa 129631


 Score = 60.0 bits (30), Expect = 1e-05
 Identities = 30/30 (100%)
 Strand = Plus / Plus


Query: 1167   tgtgttacctgctccagaaagaccttctca 1196
              ||||||||||||||||||||||||||||||
Sbjct: 129572 tgtgttacctgctccagaaagaccttctca 129601


 Score = 60.0 bits (30), Expect = 1e-05
 Identities = 30/30 (100%)
 Strand = Plus / Plus


Query: 1137   taaatggagttattcattcatcaaaaaaca 1166
              ||||||||||||||||||||||||||||||
Sbjct: 129512 taaatggagttattcattcatcaaaaaaca 129541
```

```
 Score = 60.0 bits (30), Expect = 1e-05
 Identities = 30/30 (100%)
 Strand = Plus / Plus


Query: 691    tgggcctcaggtgaaactctctggcagcca 720
              ||||||||||||||||||||||||||||||
Sbjct: 129482 tgggcctcaggtgaaactctctggcagcca 129511


 Score = 60.0 bits (30), Expect = 1e-05
 Identities = 30/30 (100%)
 Strand = Plus / Plus


Query: 661    agaaaacagacttgaagaaaatgagatgat 690
              ||||||||||||||||||||||||||||||
Sbjct: 129422 agaaaacagacttgaagaaaatgagatgat 129451


 Score = 60.0 bits (30), Expect = 1e-05
 Identities = 30/30 (100%)
 Strand = Plus / Plus


Query: 1077   cagaagtataagctgtggattgtccaacaa 1106
              ||||||||||||||||||||||||||||||
Sbjct: 129392 cagaagtataagctgtggattgtccaacaa 129421


 Score = 60.0 bits (30), Expect = 1e-05
 Identities = 30/30 (100%)
 Strand = Plus / Plus


Query: 1047   attgctagttcagtatattctgcccttagt 1076
              ||||||||||||||||||||||||||||||
Sbjct: 129332 attgctagttcagtatattctgcccttagt 129361


 Score = 60.0 bits (30), Expect = 1e-05
 Identities = 30/30 (100%)
 Strand = Plus / Plus


Query: 601    ttcatacagaattgcctttactatctcttt 630
              ||||||||||||||||||||||||||||||
Sbjct: 129302 ttcatacagaattgcctttactatctcttt 129331


 Score = 60.0 bits (30), Expect = 1e-05
 Identities = 30/30 (100%)
 Strand = Plus / Plus
```

```
Query: 1017   gtatttatgtgttgagtcatggccatctga 1046
              ||||||||||||||||||||||||||||||
Sbjct: 129272 gtatttatgtgttgagtcatggccatctga 129301


 Score = 60.0 bits (30), Expect = 1e-05
 Identities = 30/30 (100%)
 Strand = Plus / Plus


Query: 571    aacatttggttcagcattgctgagcagcag 600
              ||||||||||||||||||||||||||||||
Sbjct: 129242 aacatttggttcagcattgctgagcagcag 129271


 Score = 60.0 bits (30), Expect = 1e-05
 Identities = 30/30 (100%)
 Strand = Plus / Plus


Query: 987    agtgtttcacagtcttgtggaacttcaaga 1016
              ||||||||||||||||||||||||||||||
Sbjct: 129212 agtgtttcacagtcttgtggaacttcaaga 129241


 Score = 54.0 bits (27), Expect = 0.001
 Identities = 27/27 (100%)
 Strand = Plus / Plus


Query: 961    gtaataattctcactgtttaccaagga 987
              |||||||||||||||||||||||||||
Sbjct: 130022 gtaataattctcactgtttaccaagga 130048


☐ >gi|1438903|gb|U56079.1|HSU56079  GU Human Y5 receptor mRNA, complete cds
          Length = 1418

 Score = 1132 bits (571), Expect = 0.0
 Identities = 571/571 (100%)
 Strand = Plus / Plus


Query: 1    ttttggttgctgacaaatgtctttttattccaagcaggactataatatggatttagagct 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 10   ttttggttgctgacaaatgtctttttattccaagcaggactataatatggatttagagct 69


Query: 61   cgacgagtattataacaagacacttgccacagagaataatactgctgccactcggaattc 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 70   cgacgagtattataacaagacacttgccacagagaataatactgctgccactcggaattc 129


Query: 121  tgatttcccagtctgggatgactataaaagcagtgtagatgacttacagtattttctgat 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```



Sequences producing significant alignments:	Score (bits)	E Value	
gi|16756377|gb|AC079238.7| Homo sapiens BAC clone RP11-719L...	1459	0.0	
gi|1438903|gb|U56079.1|HSU56079 Human Y5 receptor mRNA, com...	1459	0.0	G|U
gi|1620655|gb|U66275.1|HSU66275 Human neuropeptide Y5 recep...	1402	0.0	G|U
gi|22832895|gb|BC034224.1| Homo sapiens neuropeptide Y rece...	1386	0.0	G|U
gi|31377784|ref|NM_006174.2| Homo sapiens neuropeptide Y re...	1386	0.0	G|U E
gi|27502795|gb|BC042416.1| Homo sapiens neuropeptide Y rece...	1386	0.0	G|U
gi|1945448|gb|U94320.1|HSU94320 Human neuropeptide Y5 recep...	1386	0.0	G|U E
gi|32481996|gb|AY322538.1| Homo sapiens neuropeptide Y rece...	1368	0.0	G
gi|11875769|gb|AF303091.1|AF303091 Macaca mulatta neuropept...	1289	0.0	
gi|50978823|ref|NM_001003118.1| Canis familiaris neuropepti...	971	0.0	G|U
gi|3169282|gb|AF049328.1|AF049328 Canis familiaris neuropep...	971	0.0	G|U E
gi|14029709|gb|AF363240.1|AF363240 Cavia porcellus NPY rece...	932	0.0	
gi|22476189|gb|AC123796.2| Mus musculus BAC clone RP24-320P...	692	0.0	
gi|33942177|gb|AC116731.9| Mus musculus chromosome 8, clone...	692	0.0	
gi|52839799|gb|AC100541.17| Mus musculus chromosome 8, clon...	692	0.0	

gi|2564650|gb|AF022948.1|AF022948 Mus musculus neuropeptide...	692	0.0	G
gi|26337480|dbj|AK045587.1| Mus musculus adult male corpora...	692	0.0	G U
gi|7710071|ref|NM_016708.1| Mus musculus neuropeptide Y rec...	684	0.0	G U E
gi|6714644|dbj|AB001346.1| Mus musculus mRNA for neuropepti...	684	0.0	G U E
gi|3169284|gb|AF049329.1|AF049329 Mus musculus neuropeptide...	684	0.0	G U E
gi|6981283|ref|NM_012869.1| Rattus norvegicus neuropeptide ...	672	0.0	G U E
gi|1620657|gb|U66274.1|RNU66274 Rattus norvegicus neuropept...	672	0.0	G U E
gi|1438905|gb|U56078.1|RNU56078 Rattus norvegicus Y5 recept...	672	0.0	G U
gi|3098509|gb|AF044264.1|AF044264 Rattus norvegicus neurope...	672	0.0	G U
gi|4249728|gb|AF106083.1|AF106083 Sus scrofa neuropeptide Y...	668	0.0	
gi|3808059|dbj|AB019185.1| Sus scrofa NPY Y5 gene for neuro...	668	0.0	
gi|976208|gb|L47169.1|HUMNPYAC Homo sapiens neuropeptide Y ...	460	e-126	
gi|41350310|ref|NM_000909.4| Homo sapiens neuropeptide Y re...	125	2e-25	G U
gi|47939538|gb|BC071720.1| Homo sapiens neuropeptide Y rece...	125	2e-25	G U
gi|34194271|gb|BC036657.2| Homo sapiens neuropeptide Y rece...	125	2e-25	G U
gi|45239064|gb|AY548168.1| Homo sapiens neuropeptide Y1 rec...	125	2e-25	G U
gi|1430810|emb|X99269.1|HSNPYY1 H.sapiens NPYY1 gene	125	2e-25	G
gi|189155|gb|M88461.1|HUMNEYPEPY Human neuropeptide Y pepti...	125	2e-25	G U E
gi|189284|gb|L07615.1|HUMNPYY1A2 Human neuropeptide Y recep...	125	2e-25	G U E
gi|189153|gb|M84755.1|HUMNEUYREC Human neuropeptide y recep...	125	2e-25	G U E
gi|11875765|gb|AF303089.1|AF303089 Macaca mulatta neuropept...	117	6e-23	
gi|50950122|ref|NM_001002930.1| Canis familiaris neuropepti...	109	1e-20	G U
gi|2988393|gb|AF005778.1|AF005778 Canis familiaris neuropep...	109	1e-20	G U E
gi|5410445|gb|AF135061.1|AF135061 Cavia porcellus neuropept...	103	8e-19	
gi|50746171|ref|XM_420388.1| PREDICTED: Gallus gallus simil...	98	5e-17	G
gi|47523647|ref|NM_214288.1| Sus scrofa neuropeptide Y Y1 r...	96	2e-16	G U
gi|6457647|gb|AF106081.2|AF106081 Sus scrofa neuropeptide Y...	96	2e-16	G
gi|9789708|gb|AF005779.2|AF005779 Sus scrofa neuropeptide Y...	96	2e-16	G U
gi|19548983|gb|AY040844.1| Gallus gallus neuropeptide Y rec...	92	3e-15	
gi|34877857|ref|XM_344502.1| Rattus norvegicus neuropeptide...	76	2e-10	G U
gi|30410855|gb|BC051420.1| Mus musculus neuropeptide Y rece...	76	2e-10	G U
gi|6754881|ref|NM_010934.1| Mus musculus neuropeptide Y rec...	76	2e-10	G U E
gi|53442|emb|Z18283.1|MMNPY1E03 Mus musculus of NPY-1 recep...	76	2e-10	G
gi|57636|emb|Z11504.1|RRNPV1R R.rattus mRNA for NPY-1 receptor	76	2e-10	G E
gi|53438|emb|Z18280.1|MMNPY1CDS Mus musculus NPY-1 receptor	76	2e-10	G E
gi|961479|dbj|D63819.1|MUSNYY1RB Mouse mRNA for neuropeptid...	76	2e-10	G U E
gi|961477|dbj|D63818.1|MUSNYY1RA Mouse mRNA for neuropeptid...	76	2e-10	G U E
gi|50746251|ref|XM_426285.1| PREDICTED: Gallus gallus simil...	64	7e-07	G
gi|19548985|gb|AY040845.1| Gallus gallus neuropeptide Y rec...	64	7e-07	
gi|409169|gb|L25416.1|XELNPYPYY Xenopus laevis NPY/PYY rece...	64	7e-07	G U
gi|46427829|emb|CR389184.1| Gallus gallus finished cDNA, cl...	56	2e-04	U
gi|33302262|gb|AY177273.1|AY177272S2 Squalus acanthias NPY ...	56	2e-04	
gi|1480713|gb|U62122.1|OAU62122 Ovis aries Y1 neuropeptide ...	56	2e-04	G U
gi|18425235|gb|AC093027.12| Homo sapiens 12q BAC RP11-701B6...	48	0.042	
gi|51988057|gb|AC123647.9| Mus musculus chromosome 3, clone...	44	0.66	
gi|51100952|dbj|AB104827.2| Candida boidinii FGH1 gene for ...	44	0.66	
gi|31746714|gb|AC133101.4| Mus musculus BAC clone RP23-154M...	42	2.6	
gi|37693674|gb|AC121082.13| Mus musculus chromosome 7, clon...	42	2.6	
gi|53379715|gb|AC149588.4| Mus musculus chromosome 15 clone...	42	2.6	

gi|52077841|gb|AC132394.3|	Mus musculus chromosome 6 clone ...	42	2.6	
gi|49533628|gb|AC115341.6|	Rattus norvegicus 3 BAC CH230-24...	42	2.6	
gi|20334476|gb|AC079822.13|	Homo sapiens 3 BAC RP11-413G22 ...	42	2.6	
gi|20986479|gb|AC084701.5|	Homo sapiens chromosome 18, clon...	42	2.6	
gi|2462139|emb|Z70681.1|CEC30F2	Caenorhabditis elegans cosm...	42	2.6	
gi|28144384|gb|AC008443.10|	Homo sapiens chromosome 5 clone...	42	2.6	
gi|27228882|gb|AC104463.3|	Homo sapiens chromosome 1 clone ...	42	2.6	
gi|26080542|gb|AC098934.3|	Homo sapiens chromosome 1 clone ...	42	2.6	
gi|4753229|gb|AC006335.2|AC006335	Homo sapiens BAC clone RP...	42	2.6	
gi|15431133|gb|AC013660.9|	Homo sapiens, clone RP11-20A14, ...	42	2.6	
gi|7408112|gb|AC017019.3|AC017019	Homo sapiens BAC clone RP...	42	2.6	
gi|608510|gb|U16311.1|BRU16311	Brachydanio rerio homeodomai...	42	2.6	G|U
gi|26330583|dbj|AK035302.1|	Mus musculus adult male urinary...	42	2.6	G|U
gi|26084230|dbj|AK034836.1|	Mus musculus 12 days embryo emb...	42	2.6	G|U
gi|21655430|emb|AL732316.10|	Mouse DNA sequence from clone ...	42	2.6	
gi|38678612|gb|AC117702.10|	Mus musculus chromosome 10, clo...	40	10	
gi|17570664|ref|NM_077495.1|	Caenorhabditis elegans allatos...	40	10	G
gi|22539392|gb|AC114918.4|	Mus musculus BAC clone RP23-86N2...	40	10	
gi|33242564|gb|AY336522.1|	Sulfolobus solfataricus strain P...	40	10	
gi|51854744|gb|AC133187.3|	Mus musculus chromosome 1 clone ...	40	10	
gi|44844336|emb|BX247953.2|	Mouse DNA sequence from clone R...	40	10	
gi|51233561|gb|AC110499.19|	Mus musculus chromosome 1, clon...	40	10	
gi|50902420|gb|CP000003.1|	Streptococcus pyogenes MGAS10394...	40	10	
gi|50761406|ref|XM_424720.1|	PREDICTED: Gallus gallus simil...	40	10	G
gi|21904646|gb|AE014155.1|	Streptococcus pyogenes MGAS315, ...	40	10	
gi|34786898|emb|AL831812.5|CNS08CAP	Oryza sativa chromosome...	40	10	
gi|21535755|emb|AL713907.3|CNS07YQ7	Oryza sativa chromosome...	40	10	
gi|33620400|emb|AL929018.14|	Mouse DNA sequence from clone ...	40	10	
gi|21281541|gb|AC104163.2|	Homo sapiens chromosome 3 clone ...	40	10	
gi|21206336|gb|AC100868.2|	Homo sapiens chromosome 8, clone...	40	10	
gi|27228874|gb|AC093576.3|	Homo sapiens chromosome 1 clone ...	40	10	
gi|51534200|emb|BX530059.4|	Zebrafish DNA sequence from clo...	40	10	
gi|21104611|dbj|AP003241.3|	Oryza sativa (japonica cultivar...	40	10	
gi|15623809|dbj|AP003231.3|	Oryza sativa (japonica cultivar...	40	10	
gi|25137544|dbj|AP005900.1|	Homo sapiens genomic DNA, chrom...	40	10	
gi|46240964|gb|AC145942.4|	Gallus gallus chromosome UNK clo...	40	10	

Alignments

Get selected sequences | Select all | Deselect all

☐ >gi|16756377|gb|AC079238.7| D Homo sapiens BAC clone RP11-719L21 from 4, complet
Length = 142462

Score = 1459 bits (736), Expect = 0.0
Identities = 750/752 (99%), Gaps = 2/752 (0%)
Strand = Plus / Plus

```
Query: 1      ttttggttgctgacaaatgtctttttattccaagcaggactataatatggatttagagct 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 128642 ttttggttgctgacaaatgtctttttattccaagcaggactataatatggatttagagct 128701


Query: 61     cgacgagtattataacaagacacttgccacagagaataatactgctgccactcggaattc 120
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 128702 cgacgagtattataacaagacacttgccacagagaataatactgctgccactcggaattc 128761


Query: 121    tgatttcccagtctgggatgactataaaagcagtgtagatgacttacagtattttctgat 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 128762 tgatttcccagtctgggatgactataaaagcagtgtagatgacttacagtattttctgat 128821


Query: 181    tgggctctatacatttgtaagtcttcttggctttatggggaatctacttattttaatggc 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 128822 tgggctctatacatttgtaagtcttcttggctttatggggaatctacttattttaatggc 128881


Query: 241    tctcatgaaaaagcgtaatcagaagactacggtaaacttcctcataggcaatctggcctt 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 128882 tctcatgaaaaagcgtaatcagaagactacggtaaacttcctcataggcaatctggcctt 128941


Query: 301    ttctgatatcttggttgtgctgttttgctcacctttcacactgacgtctgtcttgctgga 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 128942 ttctgatatcttggttgtgctgttttgctcacctttcacactgacgtctgtcttgctgga 129001


Query: 361    tcagtggatgtttggcaaagtcatgtgccatattatgccttttcttcaatgtgtgtcagt 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 129002 tcagtggatgtttggcaaagtcatgtgccatattatgccttttcttcaatgtgtgtcagt 129061


Query: 421    tttggtttcaactttaattttaatatcaattgccattgtcaggtatcatatgataaaaca 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 129062 tttggtttcaactttaattttaatatcaattgccattgtcaggtatcatatgataaaaca 129121


Query: 481    tcccatatctaataatttaacagcaaaccatggctactttctgatagctactgtctggac 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 129122 tcccatatctaataatttaacagcaaaccatggctactttctgatagctactgtctggac 129181


Query: 541    actaggttttgccatctgttctcccccttccagtgtttcacagtcttgtggaacttcaaga 600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 129182 actaggttttgccatctgttctcccccttccagtgtttcacagtcttgtggaacttcaaga 129241


Query: 601    aacatttggttcagcattgct-agcagcaggtatttatgtgttgagtcatggccatctga 659
               |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct: 129242 aacatttggttcagcattgctgagcagcaggtatttatgtgttgagtcatggccatctga 129301


Query: 660    ttcatacagaattgcctttactatctctttattgctagttcagt-tattctgcccttagt 718
               |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct: 129302 ttcatacagaattgcctttactatctctttattgctagttcagtatattctgcccttagt 129361


Query: 719    ttgtcttactgtaagtcatacaagtgtctgca 750
               |||||||||||||||||||||||||||||||
Sbjct: 129362 ttgtcttactgtaagtcatacaagtgtctgca 129393
```

[redacted]

```
 Score =  505 bits (255), Expect = e-140
 Identities = 255/255 (100%)
 Strand = Plus / Plus


Query: 813    agatctcgaagtgttttctacagactgaccatactgatattagtatttgctgttagttgg 872
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 129771 agatctcgaagtgttttctacagactgaccatactgatattagtatttgctgttagttgg 129830


Query: 873    atgccactacacctttccatgtggtaactgattttaatgacaatcttatttcaaatagg 932
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 129831 atgccactacacctttccatgtggtaactgattttaatgacaatcttatttcaaatagg 129890


Query: 933    catttcaagttggtgtattgcatttgtcatttgttgggcatgatgtcctgttgtcttaat 992
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 129891 catttcaagttggtgtattgcatttgtcatttgttgggcatgatgtcctgttgtcttaat 129950


Query: 993    ccaattctatatgggtttcttaataatgggattaaagctgatttagtgtcccttatacac 1052
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 129951 ccaattctatatgggtttcttaataatgggattaaagctgatttagtgtcccttatacac 130010


Query: 1053   tgtcttcatatgtaa 1067
              |||||||||||||||
Sbjct: 130011 tgtcttcatatgtaa 130025


 Score =  125 bits (63), Expect = 2e-25
 Identities = 63/63 (100%)
 Strand = Plus / Minus


Query: 750    atacgcctaaaaaggagaaacaacatgatggacaagatgagagacaataagtacaggtcc 809
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 104166 atacgcctaaaaaggagaaacaacatgatggacaagatgagagacaataagtacaggtcc 104107


Query: 810    agt 812
              |||
Sbjct: 104106 agt 104104


☐ >gi|1438903|gb|U56079.1|HSU56079  GU  Human Y5 receptor mRNA, complete cds
          Length = 1418

 Score = 1459 bits (736), Expect = 0.0
 Identities = 750/752 (99%), Gaps = 2/752 (0%)
 Strand = Plus / Plus


Query: 1    ttttggttgctgacaaatgtctttttattccaagcaggactataatatggatttagagct 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 10   ttttggttgctgacaaatgtctttttattccaagcaggactataatatggatttagagct 69
```

```
Query: 61   cgacgagtattataacaagacacttgccacagagaataatactgctgccactcggaattc 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 70   cgacgagtattataacaagacacttgccacagagaataatactgctgccactcggaattc 129

Query: 121  tgatttcccagtctgggatgactataaaagcagtgtagatgacttacagtattttctgat 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 130  tgatttcccagtctgggatgactataaaagcagtgtagatgacttacagtattttctgat 189

Query: 181  tgggctctatacatttgtaagtcttcttggctttatggggaatctacttattttaatggc 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 190  tgggctctatacatttgtaagtcttcttggctttatggggaatctacttattttaatggc 249

Query: 241  tctcatgaaaaagcgtaatcagaagactacggtaaacttcctcataggcaatctggcctt 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 250  tctcatgaaaaagcgtaatcagaagactacggtaaacttcctcataggcaatctggcctt 309

Query: 301  ttctgatatcttggttgtgctgttttgctcacctttcacactgacgtctgtcttgctgga 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 310  ttctgatatcttggttgtgctgttttgctcacctttcacactgacgtctgtcttgctgga 369

Query: 361  tcagtggatgtttggcaaagtcatgtgccatattatgccttttcttcaatgtgtgtcagt 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 370  tcagtggatgtttggcaaagtcatgtgccatattatgccttttcttcaatgtgtgtcagt 429

Query: 421  tttggtttcaactttaattttaatatcaattgccattgtcaggtatcatatgataaaaca 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 430  tttggtttcaactttaattttaatatcaattgccattgtcaggtatcatatgataaaaca 489

Query: 481  tcccatatctaataatttaacagcaaaccatggctactttctgatagctactgtctggac 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 490  tcccatatctaataatttaacagcaaaccatggctactttctgatagctactgtctggac 549

Query: 541  actaggttttgccatctgttctccccttccagtgtttcacagtcttgtggaacttcaaga 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 550  actaggttttgccatctgttctccccttccagtgtttcacagtcttgtggaacttcaaga 609

Query: 601  aacatttggttcagcattgct-agcagcaggtatttatgtgttgagtcatggccatctga 659
             |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct: 610  aacatttggttcagcattgctgagcagcaggtatttatgtgttgagtcatggccatctga 669

Query: 660  ttcatacagaattgcctttactatctctttattgctagttcagt-tattctgcccttagt 718
             |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct: 670  ttcatacagaattgcctttactatctctttattgctagttcagtatattctgcccttagt 729

Query: 719  ttgtcttactgtaagtcatacaagtgtctgca 750
             |||||||||||||||||||||||||||||||
Sbjct: 730  ttgtcttactgtaagtcatacaagtgtctgca 761
```

[redacted]

```
 Score =  505 bits (255), Expect = e-140
 Identities = 255/255 (100%)
 Strand = Plus / Plus


Query: 813  agatctcgaagtgttttctacagactgaccatactgatattagtatttgctgttagttgg 872
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1139 agatctcgaagtgttttctacagactgaccatactgatattagtatttgctgttagttgg 1198


Query: 873  atgccactacacctttccatgtggtaactgattttaatgacaatcttatttcaaatagg 932
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1199 atgccactacacctttccatgtggtaactgattttaatgacaatcttatttcaaatagg 1258


Query: 933  catttcaagttggtgtattgcatttgtcatttgttgggcatgatgtcctgttgtcttaat 992
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1259 catttcaagttggtgtattgcatttgtcatttgttgggcatgatgtcctgttgtcttaat 1318


Query: 993  ccaattctatatgggtttcttaataatgggattaaagctgatttagtgtcccttatacac 1052
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1319 ccaattctatatgggtttcttaataatgggattaaagctgatttagtgtcccttatacac 1378


Query: 1053 tgtcttcatatgtaa 1067
          |||||||||||||||
Sbjct: 1379 tgtcttcatatgtaa 1393
```

☐ >gi|1620655|gb|U66275.1|HSU66275 GU Human neuropeptide Y5 receptor (NPYR5) mRNA
Length = 1370

```
 Score = 1402 bits (707), Expect = 0.0
 Identities = 721/723 (99%), Gaps = 2/723 (0%)
 Strand = Plus / Plus


Query: 30   ccaagcaggactataatatggatttagagctcgacgagtattataacaagacacttgcca 89
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1    ccaagcaggactataatatggatttagagctcgacgagtattataacaagacacttgcca 60


Query: 90   cagagaataatactgctgccactcggaattctgatttcccagtctgggatgactataaaa 149
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 61   cagagaataatactgctgccactcggaattctgatttcccagtctgggatgactataaaa 120


Query: 150  gcagtgtagatgacttacagtattttctgattgggctctatacatttgtaagtcttcttg 209
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 121  gcagtgtagatgacttacagtattttctgattgggctctatacatttgtaagtcttcttg 180


Query: 210  gctttatggggaatctacttattttaatggctctcatgaaaaagcgtaatcagaagacta 269
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 181  gctttatggggaatctacttattttaatggctctcatgaaaaagcgtaatcagaagacta 240
```

```
Query: 270 cggtaaacttcctcataggcaatctggccttttctgatatcttggttgtgctgttttgct 329
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 241 cggtaaacttcctcataggcaatctggccttttctgatatcttggttgtgctgttttgct 300


Query: 330 caccttttcacactgacgtctgtcttgctggatcagtggatgtttggcaaagtcatgtgcc 389
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 301 caccttttcacactgacgtctgtcttgctggatcagtggatgtttggcaaagtcatgtgcc 360


Query: 390 atattatgccttttcttcaatgtgtgtcagttttggtttcaactttaattttaatatcaa 449
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 361 atattatgccttttcttcaatgtgtgtcagttttggtttcaactttaattttaatatcaa 420


Query: 450 ttgccattgtcaggtatcatatgataaaacatcccatatctaataatttaacagcaaacc 509
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 421 ttgccattgtcaggtatcatatgataaaacatcccatatctaataatttaacagcaaacc 480


Query: 510 atggctactttctgatagctactgtctggacactaggttttgccatctgttctcccccttc 569
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 481 atggctactttctgatagctactgtctggacactaggttttgccatctgttctcccccttc 540


Query: 570 cagtgtttcacagtcttgtggaacttcaagaaacatttggttcagcattgct-agcagca 628
           |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct: 541 cagtgtttcacagtcttgtggaacttcaagaaacatttggttcagcattgctgagcagca 600


Query: 629 ggtatttatgtgttgagtcatggccatctgattcatacagaattgcctttactatctctt 688
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 601 ggtatttatgtgttgagtcatggccatctgattcatacagaattgcctttactatctctt 660


Query: 689 tattgctagttcagt-tattctgcccttagtttgtcttactgtaagtcatacaagtgtct 747
           |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 661 tattgctagttcagtatattctgcccttagtttgtcttactgtaagtcatacaagtgtct 720


Query: 748 gca 750
           |||
Sbjct: 721 gca 723
```

Score = 505 bits (255), Expect = e-140
Identities = 255/255 (100%)
Strand = Plus / Plus

```
Query: 813  agatctcgaagtgttttctacagactgaccatactgatattagtatttgctgttagttgg 872
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1101 agatctcgaagtgttttctacagactgaccatactgatattagtatttgctgttagttgg 1160


Query: 873  atgccactacacctttccatgtggtaactgattttaatgacaatcttatttcaaatagg 932
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1161 atgccactacacctttccatgtggtaactgattttaatgacaatcttatttcaaatagg 1220
```

```
Query: 933  catttcaagttggtgtattgcatttgtcatttgttgggcatgatgtcctgttgtcttaat 992
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1221 catttcaagttggtgtattgcatttgtcatttgttgggcatgatgtcctgttgtcttaat 1280


Query: 993  ccaattctatatgggtttcttaataatgggattaaagctgatttagtgtcccttatacac 1052
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1281 ccaattctatatgggtttcttaataatgggattaaagctgatttagtgtcccttatacac 1340


Query: 1053 tgtcttcatatgtaa 1067
          |||||||||||||||
Sbjct: 1341 tgtcttcatatgtaa 1355
```

☐ >gi|22832895|gb|BC034224.1| G|U Homo sapiens neuropeptide Y receptor Y5, mRNA (c
IMAGE:4838926), partial cds
Length = 3197

```
 Score = 1386 bits (699), Expect = 0.0
 Identities = 713/715 (99%), Gaps = 2/715 (0%)
 Strand = Plus / Plus


Query: 38   gactataatatggatttagagctcgacgagtattataacaagacacttgccacagagaat 97
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1514 gactataatatggatttagagctcgacgagtattataacaagacacttgccacagagaat 1573


Query: 98   aatactgctgccactcggaattctgatttcccagtctgggatgactataaaagcagtgta 157
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1574 aatactgctgccactcggaattctgatttcccagtctgggatgactataaaagcagtgta 1633


Query: 158  gatgacttacagtattttctgattgggctctatacatttgtaagtcttcttggctttatg 217
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1634 gatgacttacagtattttctgattgggctctatacatttgtaagtcttcttggctttatg 1693


Query: 218  gggaatctacttattttaatggctctcatgaaaaagcgtaatcagaagactacggtaaac 277
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1694 gggaatctacttattttaatggctctcatgaaaaagcgtaatcagaagactacggtaaac 1753


Query: 278  ttcctcataggcaatctggccttttctgatatcttggttgtgctgttttgctcacctttc 337
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1754 ttcctcataggcaatctggccttttctgatatcttggttgtgctgttttgctcacctttc 1813


Query: 338  acactgacgtctgtcttgctggatcagtggatgtttggcaaagtcatgtgccatattatg 397
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1814 acactgacgtctgtcttgctggatcagtggatgtttggcaaagtcatgtgccatattatg 1873


Query: 398  ccttttcttcaatgtgtgtcagttttggtttcaactttaattttaatatcaattgccatt 457
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1874 ccttttcttcaatgtgtgtcagttttggtttcaactttaattttaatatcaattgccatt 1933
```